

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/781,989
Source: 1'FWO
Date Processed by STIC: 5/18/05

ENTERED



IFWO

RAW SEQUENCE LISTING

DATE: 05/18/2005

PATENT APPLICATION: US/10/781,989

TIME: 11:23:38

Input Set : A:\SEQLIST41514-2000303.TXT

Output Set: N:\CRF4\05182005\J781989.raw

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4 <110> APPLICANT: HIATT, Andrew C.
5     MA, Julian K.-C.
6     LEHNER, Thomas
8 <120> TITLE OF INVENTION: METHODS FOR PRODUCING IMMUNOGLOBULINS
9     CONTAINING PROTECTION PROTEINS IN PLANTS AND THEIR USE
12 <130> FILE REFERENCE: 415142000303
14 <140> CURRENT APPLICATION NUMBER: 10/781,989
15 <141> CURRENT FILING DATE: 2004-02-18
17 <150> PRIOR APPLICATION NUMBER: 08/434,000
18 <151> PRIOR FILING DATE: 1995-05-04
20 <150> PRIOR APPLICATION NUMBER: 08/367,395
21 <151> PRIOR FILING DATE: 1994-12-30
23 <160> NUMBER OF SEQ ID NOS: 19
25 <170> SOFTWARE: FastSEQ for Windows Version 4.0
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 3517
29 <212> TYPE: DNA
30 <213> ORGANISM: Rabbit
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (124)...(2445)
36 <400> SEQUENCE: 1
37 ggccgggggtt acgggctggc cagcaggctg tgcccccagag tccggtcagc aggaggggaa 60
38 gaagtggcct aaaatctctc ccgcacatcggc agcccaggcc tagtgcccta ccagccacca 120
39 gcc atg gct ctc ttc ttg ctc acc tgc ctg ctg gct gtc ttt tca gcg 168
40     Met Ala Leu Phe Leu Leu Thr Cys Leu Leu Ala Val Phe Ser Ala
41     1             5             10             15
43 gcc acg gca caa agc tcc tta ttg ggt ccc agc tcc ata ttt ggt ccc 216
44 Ala Thr Ala Gln Ser Ser Leu Leu Gly Pro Ser Ser Ile Phe Gly Pro
45     20             25             30
47 ggg gag gtg aat gtt ttg gaa ggc gac tcg gtg tcc atc aca tgc tac 264
48 Gly Glu Val Asn Val Leu Glu Gly Asp Ser Val Ser Ile Thr Cys Tyr
49     35             40             45
51 tac cca aca acc tcc gtc acc cgg cac agc cgg aag ttc tgg tgc cgg 312
52 Tyr Pro Thr Thr Ser Val Thr Arg His Ser Arg Lys Phe Trp Cys Arg
53     50             55             60
55 gaa gag gag agc ggc cgc tgc gtg acg ctt gcc tcg acc ggc tac acg 360
56 Glu Glu Glu Ser Gly Arg Cys Val Thr Leu Ala Ser Thr Gly Tyr Thr
57     65             70             75
59 tcc cag gaa tac tcc ggg aga ggc aag ctc acc gac ttc cct gat aaa 408
60 Ser Gln Glu Tyr Ser Gly Arg Gly Lys Leu Thr Asp Phe Pro Asp Lys
61     80             85             90             95
63 ggg gag ttt gtg gtg act gtt gac caa ctc acc cag aac gac tca ggg 456

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64	Gly	Glu	Phe	Val	Val	Thr	Val	Asp	Gln	Leu	Thr	Gln	Asn	Asp	Ser	Gly	
65					100					105					110		
67	agc	tac	aag	tgt	ggc	gtg	gga	gtc	aac	ggc	cgt	ggc	ctg	gac	ttc	ggt	504
68	Ser	Tyr	Lys	Cys	Gly	Val	Gly	Val	Asn	Gly	Arg	Gly	Leu	Asp	Phe	Gly	
69				115					120					125			
71	gtc	aac	gtg	ctg	gtc	agc	cag	aag	cca	gag	cct	gat	gac	gtt	gtt	tac	552
72	Val	Asn	Val	Leu	Val	Ser	Gln	Lys	Pro	Glu	Pro	Asp	Asp	Val	Val	Tyr	
73				130					135					140			
75	aaa	caa	tat	gag	agt	tat	aca	gta	acc	atc	acc	tgc	cct	ttc	aca	tat	600
76	Lys	Gln	Tyr	Glu	Ser	Tyr	Thr	Val	Thr	Ile	Thr	Cys	Pro	Phe	Thr	Tyr	
77		145					150					155					
79	gcg	act	agg	caa	cta	aag	aag	tcc	ttt	tac	aag	gtg	gaa	gac	ggg	gaa	648
80	Ala	Thr	Arg	Gln	Leu	Lys	Lys	Ser	Phe	Tyr	Lys	Val	Glu	Asp	Gly	Glu	
81	160					165					170				175		
83	ctt	gta	ctc	atc	att	gat	tcc	agc	agt	aag	gag	gca	aag	gac	ccc	agg	696
84	Leu	Val	Leu	Ile	Ile	Asp	Ser	Ser	Ser	Ser	Lys	Glu	Ala	Lys	Asp	Pro	Arg
85				180						185					190		
87	tat	aag	ggc	aga	ata	acg	ttg	cag	atc	caa	agt	acc	aca	gca	aaa	gaa	744
88	Tyr	Lys	Gly	Arg	Ile	Thr	Leu	Gln	Ile	Gln	Ser	Thr	Thr	Ala	Lys	Glu	
89			195						200					205			
91	ttc	aca	gtc	acc	atc	aag	cat	ttg	cag	ctc	aat	gat	gct	ggg	cag	tat	792
92	Phe	Thr	Val	Thr	Ile	Lys	His	Leu	Gln	Leu	Asn	Asp	Ala	Gly	Gln	Tyr	
93			210					215					220				
95	gtc	tgc	cag	agt	gga	agc	gac	ccc	act	gct	gaa	gaa	cag	aac	gtt	gac	840
96	Val	Cys	Gln	Ser	Gly	Ser	Asp	Pro	Thr	Ala	Glu	Glu	Gln	Asn	Val	Asp	
97		225					230					235					
99	ctc	cga	ctg	cta	act	cct	ggt	ctg	ctc	tat	gga	aac	ctg	ggg	ggc	tcg	888
100	Leu	Arg	Leu	Leu	Thr	Pro	Gly	Leu	Leu	Tyr	Gly	Asn	Leu	Gly	Gly	Ser	
101	240					245					250				255		
103	gtg	acc	ttt	gaa	tgt	gcc	ctg	gac	tct	gaa	gac	gca	aac	gcg	gta	gca	936
104	Val	Thr	Phe	Glu	Cys	Ala	Leu	Asp	Ser	Glu	Asp	Ala	Asn	Ala	Val	Ala	
105				260						265					270		
107	tcc	ttg	cgc	cag	gtt	agg	ggt	ggc	aat	gtg	gtc	att	gac	agc	cag	ggg	984
108	Ser	Leu	Arg	Gln	Val	Arg	Gly	Gly	Asn	Val	Val	Ile	Asp	Ser	Gln	Gly	
109				275					280					285			
111	aca	ata	gat	cca	gcc	ttc	gag	ggc	agg	atc	ctg	ttc	acc	aag	gct	gag	1032
112	Thr	Ile	Asp	Pro	Ala	Phe	Glu	Gly	Arg	Ile	Leu	Phe	Thr	Lys	Ala	Glu	
113			290					295					300				
115	aac	ggc	cac	ttc	agt	gta	gtg	atc	gca	ggc	ctg	agg	aag	gaa	gac	aca	1080
116	Asn	Gly	His	Phe	Ser	Val	Val	Ile	Ala	Gly	Leu	Arg	Lys	Glu	Asp	Thr	
117		305					310					315					
119	ggg	aac	tat	ctg	tgc	gga	gtc	cag	tcc	aat	ggt	cag	tct	ggg	gat	ggg	1128
120	Gly	Asn	Tyr	Leu	Cys	Gly	Val	Gln	Ser	Asn	Gly	Gln	Ser	Gly	Asp	Gly	
121	320					325					330				335		
123	ccc	acc	cag	ctt	cgg	caa	ctc	ttc	gtc	aat	gaa	gag	atc	gac	gtg	tcc	1176
124	Pro	Thr	Gln	Leu	Arg	Gln	Leu	Phe	Val	Asn	Glu	Glu	Ile	Asp	Val	Ser	
125				340						345					350		
127	cgc	agc	ccc	cct	gtg	ttg	aag	ggc	ttt	cca	gga	ggc	tcc	gtg	acc	ata	1224
128	Arg	Ser	Pro	Pro	Val	Leu	Lys	Gly	Phe	Pro	Gly	Gly	Ser	Val	Thr	Ile	

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129		355		360		365		
131	cgc tgc ccc	tac aac ccg aag aga agc gac agc cac	ctg cag ctg tat	1272				
132	Arg Cys Pro	Tyr Asn Pro Lys Arg Ser Asp Ser His	Leu Gln Leu Tyr					
133		370		375		380		
135	ctc tgg gaa	ggg agt caa acc cgc cat ctg ctg gtg gac agc ggc	gag	1320				
136	Leu Trp Glu	Gly Ser Gln Thr Arg His Leu Leu Val Asp Ser Gly	Glu					
137		385		390		395		
139	ggg ctg gtt	cag aaa gac tac aca ggc agg ctg gcc ctg ttc gaa	gag	1368				
140	Gly Leu Val	Gln Lys Asp Tyr Thr Gly Arg Leu Ala Leu Phe	Glu Glu					
141	400		405		410		415	
143	cct ggc aat	ggc acc ttc tca gtc gtc ctc aac cag ctc act gcc	gag	1416				
144	Pro Gly Asn	Gly Thr Phe Ser Val Val Leu Asn Gln Leu Thr Ala	Glu					
145		420		425		430		
147	gat gaa ggc	ttc tac tgg tgt gtc agc gat gac gat gag tcc ctg	acg	1464				
148	Asp Glu Gly	Phe Tyr Trp Cys Val Ser Asp Asp Asp Glu Ser Leu	Thr					
149		435		440		445		
151	act tcg gtg	aag ctc cag atc gtt gac gga gaa cca agc ccc acg	atc	1512				
152	Thr Ser Val	Lys Leu Gln Ile Val Asp Gly Glu Pro Ser Pro Thr	Ile					
153		450		455		460		
155	gac aag ttc	act gct gtg cag gga gag cct gtt gag atc acc tgc	cac	1560				
156	Asp Lys Phe	Thr Ala Val Gln Gly Glu Pro Val Glu Ile Thr Cys	His					
157		465		470		475		
159	ttc cca tgc	aaa tac ttc tcc tcc gag aag tac tgg tgc aag tgg	aat	1608				
160	Phe Pro Cys	Lys Tyr Phe Ser Ser Glu Lys Tyr Trp Cys Lys Trp	Asn					
161	480		485		490		495	
163	gac cat ggc	tgc gag gac ctg ccc act aag ctc agc tcc agc ggc	gac	1656				
164	Asp His Gly	Cys Glu Asp Leu Pro Thr Lys Leu Ser Ser Ser Gly	Asp					
165		500		505		510		
167	ctt gtg aaa	tgc aac aac aac ctg gtc ctc acc ctg acc ttg	gac tcg	1704				
168	Leu Val Lys	Cys Asn Asn Asn Leu Val Leu Thr Leu Thr Leu Asp	Ser					
169		515		520		525		
171	gtc agc gaa	gat gac gag ggc tgg tac tgg tgt ggc gcg aaa	gac ggg	1752				
172	Val Ser Glu	Asp Asp Glu Gly Trp Tyr Trp Cys Gly Ala Lys Asp	Gly					
173		530		535		540		
175	cac gag ttt	gaa gag gtt gcg gcc gtc agg gtg gag ctg aca	gag cca	1800				
176	His Glu Phe	Glu Glu Val Ala Ala Val Arg Val Glu Leu Thr Glu	Pro					
177		545		550		555		
179	gcc aag gta	gct gtc gag cca gcc aag gta cct gtc gac cca gcc	aag	1848				
180	Ala Lys Val	Ala Val Glu Pro Ala Lys Val Pro Val Asp Pro Ala	Lys					
181	560		565		570		575	
183	gca gcc ccc	gcg cct gct gag gag aag gcc aag gcg cgg tgc cca	gtg	1896				
184	Ala Ala Pro	Ala Pro Ala Glu Glu Lys Ala Lys Ala Arg Cys Pro	Val					
185		580		585		590		
187	ccc agg aga	agg cag tgg tac cca ttg tca agg aag ctg aga aca	agt	1944				
188	Pro Arg Arg	Arg Gln Trp Tyr Pro Leu Ser Arg Lys Leu Arg Thr	Ser					
189		595		600		605		
191	tgt cca gaa	cct cgg ctc ctt gcg gag gag gta gca gtg cag	agt gcg	1992				
192	Cys Pro Glu	Pro Arg Leu Leu Ala Glu Glu Val Ala Val Gln Ser	Ala					
193		610		615		620		

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195 gaa gac cca gcc agt ggg agc aga gcg tct gtg gat gcc agc agt gct 2040
196 Glu Asp Pro Ala Ser Gly Ser Arg Ala Ser Val Asp Ala Ser Ser Ala
197      625      630      635
199 tcg gga caa agc ggg agt gcc aaa gta ctg atc tcc acc ctg gtg ccc 2088
200 Ser Gly Gln Ser Gly Ser Ala Lys Val Leu Ile Ser Thr Leu Val Pro
201 640      645      650      655
203 ttg ggg ctg gtg ctg gca gcg ggg gcc atg gcc gtg gcc ata gcc aga 2136
204 Leu Gly Leu Val Leu Ala Ala Gly Ala Met Ala Val Ala Ile Ala Arg
205      660      665      670
207 gcc cgg cac agg agg aac gtg gac cga gtt tcc atc gga agc tac agg 2184
208 Ala Arg His Arg Arg Asn Val Asp Arg Val Ser Ile Gly Ser Tyr Arg
209      675      680      685
211 aca gac att agc atg tca gac ttg gag aac tcc agg gag ttc gga gcc 2232
212 Thr Asp Ile Ser Met Ser Asp Leu Glu Asn Ser Arg Glu Phe Gly Ala
213      690      695      700
215 att gac aac cca agc gcc tgc ccc gat gcc cgg gag acg gcc ctc gga 2280
216 Ile Asp Asn Pro Ser Ala Cys Pro Asp Ala Arg Glu Thr Ala Leu Gly
217      705      710      715
219 gga aag gat gag tta gcg acg gcc acc gag agc acc gtg gag att gag 2328
220 Gly Lys Asp Glu Leu Ala Thr Ala Thr Glu Ser Thr Val Glu Ile Glu
221 720      725      730      735
223 gag ccc aag aag gca aaa cgg tca tcc aag gaa gaa gcc gac ctg gcc 2376
224 Glu Pro Lys Lys Ala Lys Arg Ser Ser Lys Glu Glu Ala Asp Leu Ala
225      740      745      750
227 tac tca gct ttc ctg ctc caa tcc aac acc ata gct gct gag cac caa 2424
228 Tyr Ser Ala Phe Leu Leu Gln Ser Asn Thr Ile Ala Ala Glu His Gln
229      755      760      765
231 gat ggc ccc aag gag gcc tag gcacagccgg ccaccgccgc cgccgccacc 2475
232 Asp Gly Pro Lys Glu Ala *
233      770
235 gccgccgccg ccgccacctg tgaaaatcac cttccagaat cacgttgatc ctcggggtcc 2535
236 ccagagccgg gggctcaacc gccctgcacc ccccatgtcc ccaccacctt aacttcccta 2595
237 cctgtgccca gaggtgtgct ggtcccctcc tccacggcat ccaggcctgg ctcaatgttc 2655
238 ccgttggggg gggggtgtga ggggttccta cttgcagccc ggttctcccg agagaagcta 2715
239 aggatccagg tcctgaggga ggggcctctc gaaggcagac agaccagaga ggggggagga 2775
240 gcccttggat gggaggccag aggcgtttc cggccacccc ctccctccct gccccacccc 2835
241 tccttccttc attcaaaagt cccagtggct gctgcctagg gtccaggcgc tggccgcacg 2895
242 cctcctcgaa gccgttgtgc aaacatcact ggaggaagcc agggctcctc ccgggctgtg 2955
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244 gtgtgccctg ggcgtgtctg caagtcaccc cagacacatg ttctcgccat tttacagatg 3075
245 agaactga ggttgactc aagggcacc tgcgagatgg agcaacagca aactagatgg 3135
246 gcttctgctg tcctcttggc cagaggtctc tccacaggag cccctgcccc tgtaggaagc 3195
247 agagttag aacatggaag aagaagaggg ggatggccct ggacgctgac ctctcccaag 3255
248 cccccacggg ggaaaaggcc ccctcctttt ctgtcactct cggggacctg cggagttgag 3315
249 cattcgtgcc ccgtgtgtct gaagagttcc cagtggaaaag aagaaaagag ggtgtttgtc 3375
250 agtgccgggg agggcctgat ccccagacag ctgaagtta aggtccttgt ccctgtgagc 3435
251 ttaaccagc acctccgggc tgacccttgc taacacatca gaaatgtgat ttaatcatta 3495
252 aacattgtga ttgccactgg ga 3517
254 <210> SEQ ID NO: 2

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255 <211> LENGTH: 773
256 <212> TYPE: PRT
257 <213> ORGANISM: Rabbit
259 <400> SEQUENCE: 2
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262 Thr Ala Gln Ser Ser Leu Leu Gly Pro Ser Ser Ile Phe Gly Pro Gly
263 20 25 30
264 Glu Val Asn Val Leu Glu Gly Asp Ser Val Ser Ile Thr Cys Tyr Tyr
265 35 40 45
266 Pro Thr Thr Ser Val Thr Arg His Ser Arg Lys Phe Trp Cys Arg Glu
267 50 55 60
268 Glu Glu Ser Gly Arg Cys Val Thr Leu Ala Ser Thr Gly Tyr Thr Ser
269 65 70 75 80
270 Gln Glu Tyr Ser Gly Arg Gly Lys Leu Thr Asp Phe Pro Asp Lys Gly
271 85 90 95
272 Glu Phe Val Val Thr Val Asp Gln Leu Thr Gln Asn Asp Ser Gly Ser
273 100 105 110
274 Tyr Lys Cys Gly Val Gly Val Asn Gly Arg Gly Leu Asp Phe Gly Val
275 115 120 125
276 Asn Val Leu Val Ser Gln Lys Pro Glu Pro Asp Asp Val Val Tyr Lys
277 130 135 140
278 Gln Tyr Glu Ser Tyr Thr Val Thr Ile Thr Cys Pro Phe Thr Tyr Ala
279 145 150 155 160
280 Thr Arg Gln Leu Lys Lys Ser Phe Tyr Lys Val Glu Asp Gly Glu Leu
281 165 170 175
282 Val Leu Ile Ile Asp Ser Ser Ser Lys Glu Ala Lys Asp Pro Arg Tyr
283 180 185 190
284 Lys Gly Arg Ile Thr Leu Gln Ile Gln Ser Thr Thr Ala Lys Glu Phe
285 195 200 205
286 Thr Val Thr Ile Lys His Leu Gln Leu Asn Asp Ala Gly Gln Tyr Val
287 210 215 220
288 Cys Gln Ser Gly Ser Asp Pro Thr Ala Glu Glu Gln Asn Val Asp Leu
289 225 230 235 240
290 Arg Leu Leu Thr Pro Gly Leu Leu Tyr Gly Asn Leu Gly Gly Ser Val
291 245 250 255
292 Thr Phe Glu Cys Ala Leu Asp Ser Glu Asp Ala Asn Ala Val Ala Ser
293 260 265 270
294 Leu Arg Gln Val Arg Gly Gly Asn Val Val Ile Asp Ser Gln Gly Thr
295 275 280 285
296 Ile Asp Pro Ala Phe Glu Gly Arg Ile Leu Phe Thr Lys Ala Glu Asn
297 290 295 300
298 Gly His Phe Ser Val Val Ile Ala Gly Leu Arg Lys Glu Asp Thr Gly
299 305 310 315 320
300 Asn Tyr Leu Cys Gly Val Gln Ser Asn Gly Gln Ser Gly Asp Gly Pro
301 325 330 335
302 Thr Gln Leu Arg Gln Leu Phe Val Asn Glu Glu Ile Asp Val Ser Arg
303 340 345 350
304 Ser Pro Pro Val Leu Lys Gly Phe Pro Gly Gly Ser Val Thr Ile Arg

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